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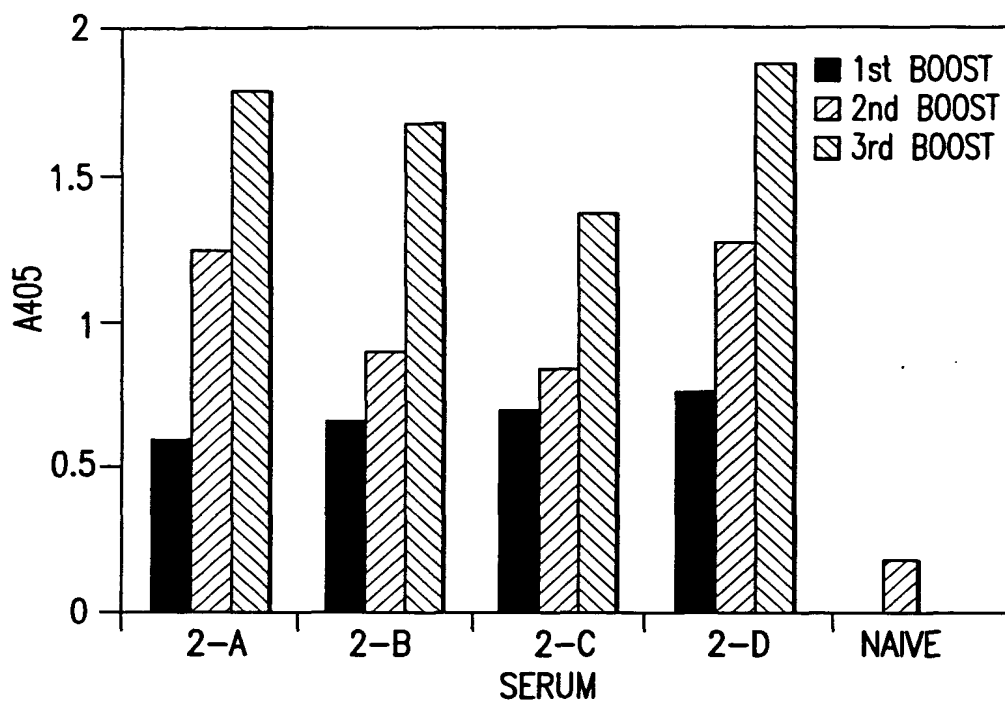


FIG.1A

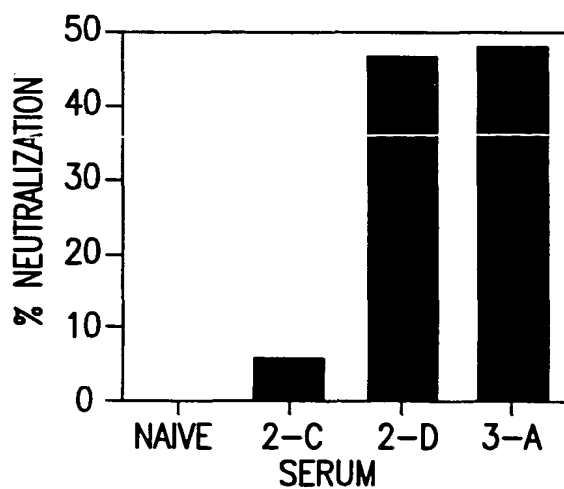
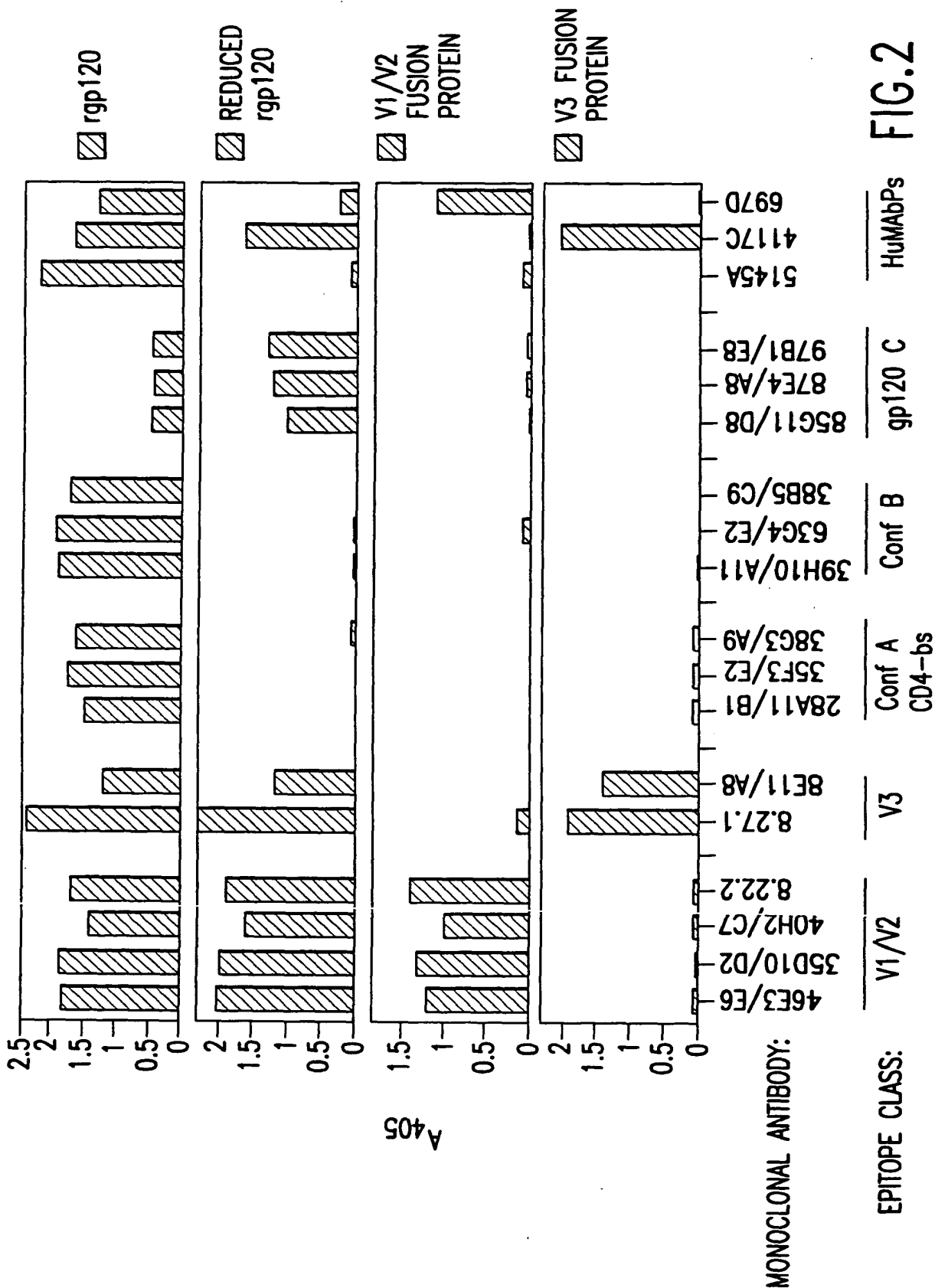
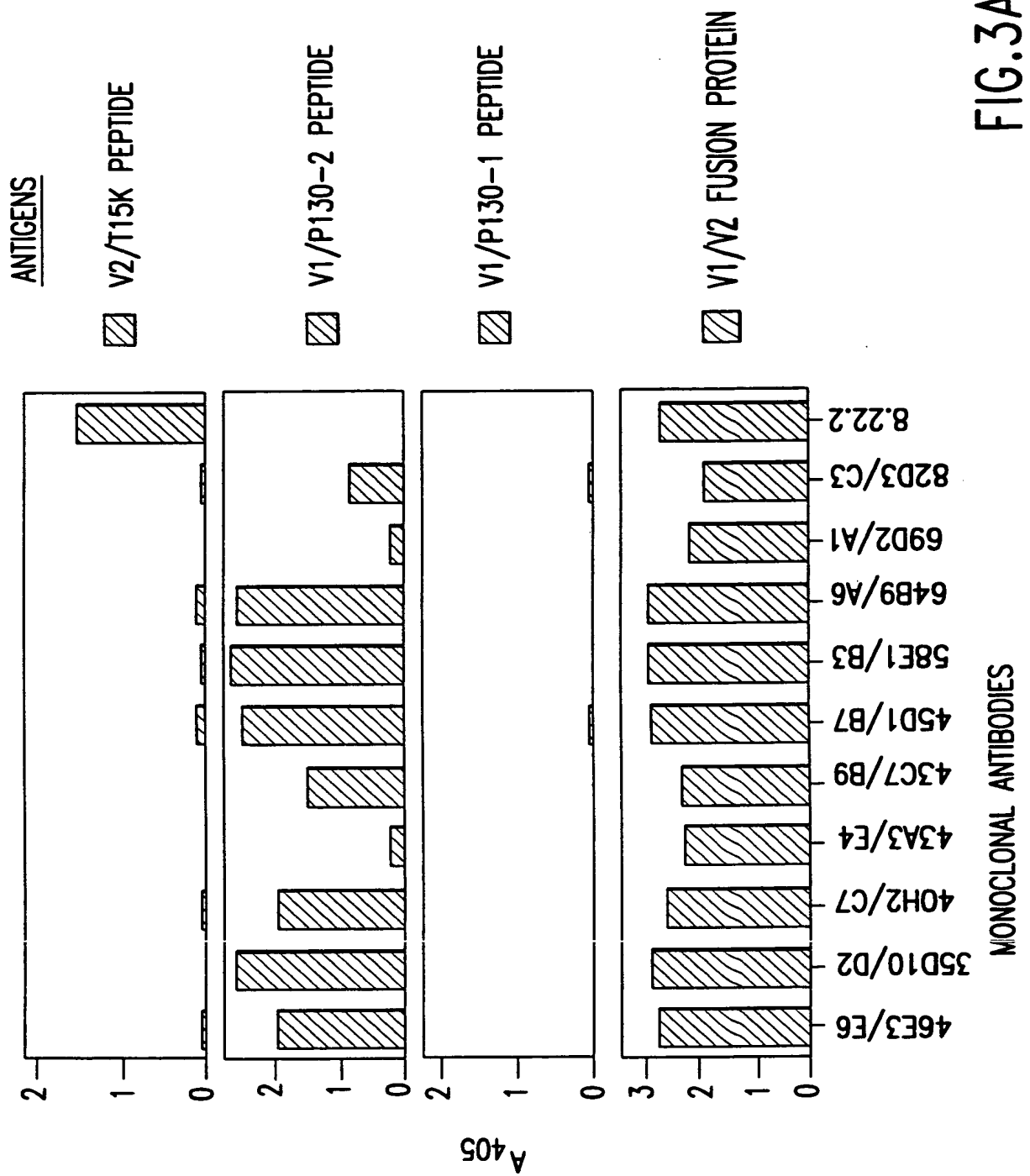


FIG.1B

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	LEFT STEM	V1	CENTRAL	V2	RIGHT STEM	
FP	LKPCVKLTPLCVTLHCTNL	KNATNTKSSNWKEMDRGEIKNCSF	KVTTSIRNKMQKEYALFYKLDVVPIDNDNTSY	KLINCNTSVITQACPKVS	SEQ ID NO: 1	
P130-1	STNL	KNATNTKSSNW			SEQ ID NO: 2	
P130-2		NTKSSNWKEMD GEIK			SEQ ID NO: 3	
T15K				TTSIRDKVQKEYALFYK	SEQ ID NO: 4	

FIG.3B

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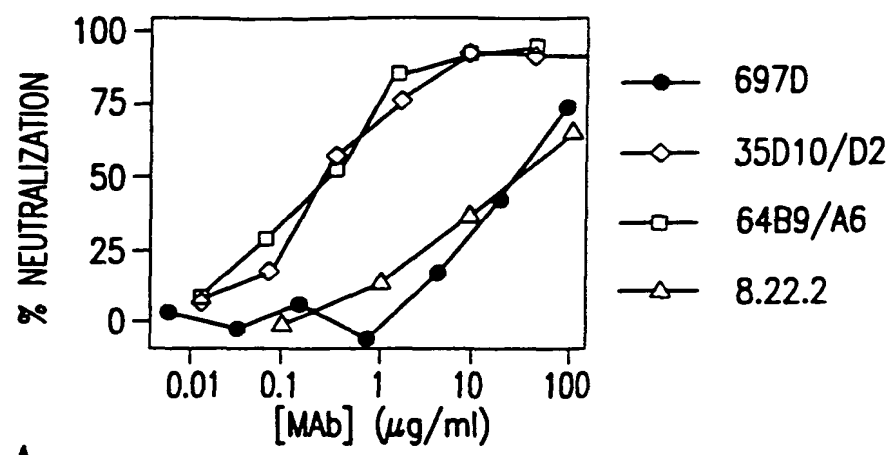


FIG. 4A

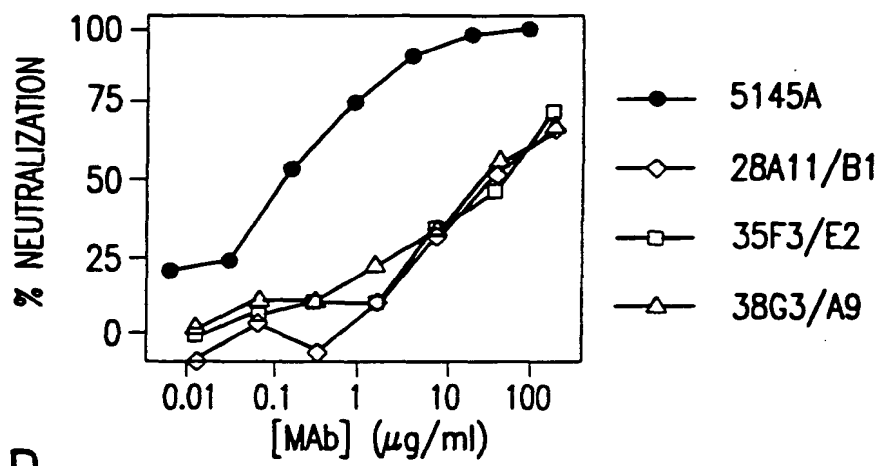


FIG. 4B

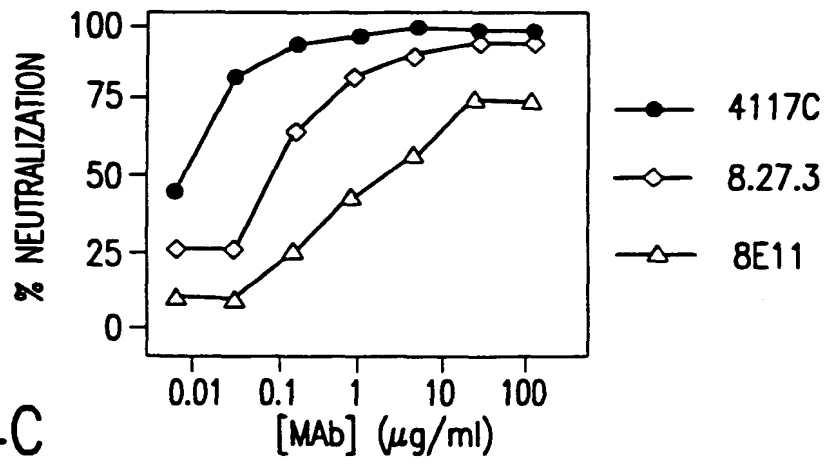


FIG. 4C

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COMPETING Mab		% INHIBITION OF BINDING BY BIOTINYLATED			
EPITOPE	NAME	43A3/E4	35D10/D2	697D	sCD4
V1 LINEAR	35D10/D2	89	89	7	26
	40H2/C7	82	83	5	13
	43A3/E4	78	82	9	10
	43C7/B9	82	83	8	13
	45D1/B7	85	85	11	17
	46E3/E6	86	86	9	-29
	58E1/B3	88	88	4	21
	64B9/A6	89	89	12	24
	69D2/A1	58	65	12	37
	82D3/C3	52	56	11	-35
V2 LINEAR	8.22.2	1	1	84	-1
V2 CONF.	697D	3	-5	83	6
	SC258	9	21	45	0
V3	8.27.3	9	24	11	9
CD4bs	5145A	0	11	-55	93

FIG. 5

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GROUP	Mob	FUSION PROTEIN				SYNTHETIC PEPTIDE				
		JR-CSF	JR-CSF	MN	Circular	MN -IIIB	IIIB	MN	11-30	MN
		Circular	Linear							
XENOMOUSE <sup>R</sup>	8E11/A8	1.94	0.98	0.82	0.88	0.95	0.01	0.01	0.69	0.01
	6.1	3.11	0.78	0.75	0.99	1.60	0.02	0.04	1.22	0.02
	6.7	3.00	0.87	0.94	0.94	1.57	0.02	0.04	1.11	0.03
Mabs	8.27.3	3.56	2.03	2.07	1.79	0.29	0.00	0.30	0.03	0.00
	694	2.03	2.20	2.56	2.00	3.36	1.99	2.72	1.72	0.05
	447-52D	2.73	2.56	2.90	2.51	3.11	1.14	3.51	0.07	0.03
HuMabPs	838	2.03	2.74	2.02	1.38	0.08	0.02	3.26	0.07	0.06
	1006	1.97	1.49	1.46	1.11	0.06	0.02	2.60	0.05	0.06
	419	1.94	1.54	2.03	1.60	0.05	0.03	1.94	0.06	0.05
E	4117C	3.08	2.96	2.90	2.84	0.13	0.09	2.53	0.12	0.12
	4148D	2.61	1.84	1.75	1.82	0.07	0.02	2.10	0.07	0.05

FIG. 6A

ISOLATE	SEQUENCE	SEQ ID NO:
SF162 (rgp120)	CTRPNNNTRKSI TIGPGRAF YATGDI IGDIRQAHC	5
JR-CSF (fusion protein)	CTRPSNNTRKSI HIGPGRAF YTTGCI IGDIRQAHC	6
MN linear	TRPNYNKRKR I HIGPGRAF YTTKNI IGTIRQAHC	7
MN circular	CTRPNNYNKRKR I HIGPGRAF YTTKNI IGTIRQAHC	8
MN 1-20	CTRPNNYNKRKR I HIGPGRAF	9
MN 11-30	RIHIGPGRAF YTTKNI IGTI	10
MN 21-40	YTTKNI IGTIRQAHCNI SRA	11
PND MN/IIIB MN 6-27 + QR	YNKRKR I HIQRGPGRAF YTTKNI I	12
HIV-1IIIB (34 aa)	TRPNNNTRKSI R IQRGPGRAF V T T G K I G N M R Q A H	13

FIG. 6B

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## % INHIBITION OF BINDING BY BIOTINYLATED

EPITOPE	COMPETING Mab	sCD4	CD4bs 38G3/A9	Conf-B 63G4/E2	gp120-C 97B1/E8
Conf A CD4bs	38G3/A9	86	91	-29	ND
	35F3/E2	86	90	-22	ND
	55D5/F9	87	85	-18	ND
	28A11/B1	82	ND	ND	ND
	46D2/D5	62	ND	ND	ND
	67G6/C4	61	ND	ND	ND
Conf B	38B5/C9	5	-32	84	ND
	39H10/A11	0	-32	91	ND
	40D3/C11	9	-26	90	ND
	49B11/A1	12	-29	90	ND
	52G5/B9	19	-37	90	ND
	56C4/C8	17	-45	88	ND
	57H5/D7	32	-15	90	ND
	63G4/E2	27	-24	91	ND
	55E4/H1	13	-46	81	-35
	57B6/F1	-1	-23	56	-34
	65B12/C5	20	-22	40	-31
gp120 C	85G11/D8*	14	-3	0	65
	87E4/A8*	20	-11	-3	70
	97B1/E8*	20	-13	-1	71
CD4bs	5145A	93	ND	ND	ND
V3	4117C	30	ND	ND	ND

FIG. 7



EPI TOPE	R5 CLADE B				X4 CLADE B			CLADE E 9/11	
	Mab	SF162	BaL	JR-FL	MN	IIIB	SF2	93TH975	CM235
V3	8.27.3	++	++	++	++	-	++	-	-
	6.7	++	+	+	+	-	-	-	-
	8E11/A8	++	+	+	+	-	-	-	-
	6.1	++	+	+	+	-	-	-	-
V1 LINEAR	35D10/D2	++	-	-	-	-	-	-	-
	40H2/C7	++	-	-	-	-	-	-	-
	43A3/E4	++	-	-	-	-	-	-	-
	43C7/B9	++	-	-	-	-	-	-	-
	45D1/B7	++	-	-	-	-	-	-	-
	46E3/E6	++	-	-	-	-	-	-	-
	58E1/B3	++	-	-	-	-	-	-	-
	64B9/A6	++	-	-	-	-	-	-	-
	69D2/A1*	+	-	-	-	-	-	-	-
	82D3/C3*	+	-	-	-	-	-	-	-
V2	8.22.2	++	++	++	-	-	-	-	-
Conf A CD4bs	28A11/B1	++	+	+	++	++	+	-	-
	35F3/E2	++	++	+	++	++	+	-	-
	38G3/A9	++	++	+	++	++	+	-	-
	55D5/F9	++	++	+	++	++	+	-	-
	46D2/D5	++	+	-	+	++	+	-	-
	67G6/C4*	+	-	-	-	-	-	-	-
Conf B	39H10/A11	++	+	+	+	++	+	+	+
	63G4/E2	++	+	+	+	++	+	+	+
	38B5/C9	++	+	+	++	++	-	+	-
	52G5/B9	++	+	+	+	++	-	+	-
	55E4/H1	++	+	+	+	++	-	+	-
	49B11/A1	++	+	+	+	++	-	+	-
	57H5/D7	++	+	+	+	+	-	+	-
	40D3/C11	++	+	+	+	++	-	+	-
	56C4/C8	++	-	+	+	++	-	+	-
	65B12/C5	+	+	-	+	+	-	-	-
gp120 C	57B6F1	++	-	-	+	+	-	-	-
	97B1/E8*	+	+	+	+	+	+	-	-
	87E4/A8*	+	+	+	+	+	-	-	-
CD4bs	85G11/D8*	+	+	-	+	-	-	-	-
	5145a	++	++	+	++	++	++	-	+

FIG.8

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EPITOPE	Mab	CROSS-REACTIVITY	SF162 ND <sub>50</sub>
NEUTRALIZING XENOMOUSE <sup>R</sup> Mabs			
V1 Linear	35D10/D2	SF162	0.27
	40H2/C7		1.9
	43A3/E4		3.2
	43C7/B9		1.4
	45D1/B7		1.9
	46E3/E6		0.30
	58E1/B3		0.55
	64B9/A6		0.29
	69D2/A1*		4.5
82D3/C3*	1.2		
V2 Linear	8.22.2	SF162 BaL JR-FL	48
V3 Linear	8E11/A8	SF162 BaL JR-FL MN	2.6
V3 Conf.	8.27.3	SF162 BaL JR-FL MN SF2	0.11
Conf. A CD4bs	28A11/B1	SF162 BaL JR-FL MN IIIB SF2	35
	35F3/E2		60
	38G3/A9		31
	55D5/F9		37
NON-NEUTRALIZING XENOMOUSE <sup>R</sup> Mabs			
V3	6.1	SF162 BaL JR-FL MN	>50
Linear	6.7		>50
Conf. A	46D2/D5	SF162 BaL MN IIIB SF2	>>200
CD4bs	67G6/C4*	SF162	>>200
Conf. B	39H10/A11	SF162 BaL JR-FL MN IIIB	>>200
	63G4/E2	SF2 93TH975 CM235	>>200
	38B5/C9		>>200
	52G5/B9		>>200
	55E4/H1	SF162 BaL JR-FL MN	>>200
	57H5/D7	IIIB 93TH975	>>200
	40D3/C11		>>200
	49B11/A1		>>200
	56C4/C8	SF162 JR-FL MN IIIB 93TH975	>>200
	57B6/F1	SF162 MN IIIB	>>200
gp120 C	65B12/C5	SF162 BaL MN IIIB	>>200
	85G11/D8*	SF162 BaL MN	>>200
	87E4/A8*	SF162 BaL JR-FL MN IIIB	>>200
	97B1/E8*	SF162 BaL JR-FL MN IIIB SF2	>>200
CONTROL HuMabPs			
CD4bs	5145a	BROADLY REACTIVE	0.14
V2 Conf.	697D	BROADLY REACTIVE	80
V3 Linear	4117c	BROADLY REACTIVE	0.02

FIG. 9

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	<u>V1</u>	<u>Central</u>	<u>V2</u>	<u>V2 stem</u>
<u>8.22.2 Reactive</u>				
SF162	HCTNLKNAATKSSNWKEMDR SEQ ID NO: 18	GEIKNCSF	KVTTSSIRNKMQKEYALFYKLDVVPIDNDNTS	YKLINC
CASEA2B	NCIDLNRNATNSNTTNTSSGGLMMEQ SEQ ID NO: 19	GEIKNCSF	NITTSIRDKVQKEYALFYKLDIVPIDNPKNSTN	YRLISC
JR-FL	NCVKDVAATNTNDSEGTMER SEQ ID NO: 20	GEIKNCSF	NITTSIRDEVQKEYALFYKLDVVPIDNNNTS	YRLISC
BaL	NCTDLRNATNGNDTNTSSSRGWGG SEQ ID NO: 21	GEMKNCSF	NITTNIRGKVQKEYALFYKLDIAPIDNNSNNR	YRLISC
<u>8.22.2 Nonreactive</u>				
HXB2d	KCTDLKNDTNTNSSGRMIMEK SEQ ID NO: 22	GEIKNCSF	NITTSIRGKVQKEYAFFYKLDIIPIDNDTTS	YKLISC
MN-ST	NCTDLRNTTNTNNSANNNSSEGTIKG SEQ ID NO: 23	GEMKNCSF	NITTSIRDKMQKEYALLYKLDIVSINDSTS	YRLISC
SF2	NCTDLGKATNTNSSNWKEEIK SEQ ID NO: 24	GEIKNCSF	NITTSIRDKIQKENALFRNLDVVPIDNASTTTNTN	YRLIHC

FIG.10